

Mouse	--MLVATLLCALCCGLLAASAHAGYSEDRCSWRGSGLTQEPGVSQGQLTLDCTEGAIEWLY	58
Rat	--MLVAALLCALCCGLLAASARAGYSEDRCSWRGSGLTQEPGVSQGQLTLDCTEGAIEWLY	58
Human	MGFPAALLCALCCGLLAPAAAGYSEERCSWRGSGLTQEPGVSQGLALACAEGAVEWLY	60
	: .*:*****.:*:*****:*****:* *.**:***	
Mouse	PAGALRLTLGGPDGPTRPSIVCLRPERPFAGAQQVFAERMGTGNLELLAEGPDLAGGRCMR	118
Rat	PAGALRLTLGGSDPGTRPSIVCLRPTRPFAGAQQVFAERMAGNLELLAEGQGLAGGRCMR	118
Human	PAGALRLTLGGPDPRARPPIACLRPVRFAGAQQVFAERAGGALELLAEGPGPAGGCVR	120
	*****.*.*.*.* ***** *	
Mouse	WGPRERRALFLQATPHRDISRRAAFRFELHEDQRAEMSPQAQGLVDGACRPCSDAELL	178
Rat	WGPRERRALFLQATPHRDISRRVAAFQFELHEDQRAEMSPQAQGFVDGACRPCSDAELL	178
Human	WGPRERRALFLQATPHQDISRRVAAFREFELREDGRPELPQAHGLVDGACRPCSDAELL	180
	*****:*****:***:* *.*.:***:*.*****	
Mouse	LAACTSDFVIHGTHIGVHADTELQESVITVVVARVIRQTPLPLFKEGSSEGQGRASIRTLL	238
Rat	LTACTSDFVIHGTHIGVVHDMELQESVITTVATRIVIRQTPLPLFQEGSSEGRQASVRTLL	238
Human	LAACTSDFVIHGIHGVTHDVELQESVITVVAARVLRTPLPLFQAGRSQDGLTSIRTPL	240
	*:***** ****.* *****.:**:* ***: * *.*: :*:*	
Mouse	RCGVPPGPSFLFMGWSRFGEAWLGCAPRFQEFSRVYSAAALTTHLNPCEMALD	291 (SEQ ID NO:26)
Rat	RCGVPPGPSFLFMGWSRFGEAWLGCAPRFQEFSRVYSAAALAHNPNCEVALD	291 (SEQ ID NO:13)
Human	RCGVHPGPGTFLFMGWSRFGEARLGCAPRFQEFRAYEAAAHLHPCEVALH	293 (SEQ ID NO:3)
	*****:*****:*****:*****:*****:*****:	

scoring matrix: BLOSUM50, gap penalties: -12/-2
42.3% identity; Global alignment score: 747

```

      10      20      30      40      50 *
Innog. MRGAARAAWGRAGQPWPRPPAPGPPPPPLLLLLLAGLLGGAG-AQYSSDRCSWKGSGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NsG33  -----MGFPAAALLCALCCGLLAPAAARAGYSEERCSSWRGSGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      10      20      30
      60      70      *      80      90      100      *110
Innog. THEAHRKEVEQVYLRCAAGAVEWMYPTGALIVNLR-PNTFSPARHLTVCAIRSFTDSSGAN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NsG33  TQEPGS--VGQLALACAEGAVEWLYPAGALRLTLGGPDPR--ARPGIACLRPVRPFAGAQA
      40      50      60      70      80      90
      120      130      140      *      150      160      170
Innog. IYLEKTG-ELRLVPDGDGRPRVQC--FG-LEQGGLFVEATPQQDIGRRTTGQYELVR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NsG33  VFAERAGGALELLLAEGPG-PAGGRCVRWGPRRRALFLQATPHQDISRRVAAFRFELRE
      100      110      120      130      140      150
      180      190      200      210      220
Innog. RHRAS--DLHELAP--CRPCSDTEVLLAVCTSDFAVRGSIQQVTHEPERQDSAIHLRV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NsG33  DGRPELPQAHGLVDGACRPCSDAELLAACTSDFVIHGIHGVTHDVELQESVITVVA
      160      170*      *      180      *      190      200      210
      230      240      250      260      270      280
Innog. SRLYRQKSRVFEPVPEGDGHWQG--RVRTLLECGVRPGHGDFLFTGHMHFGEARLGCAPR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NsG33  ARVLRQTPLPFQAGRSGD---QGLTSIRTPLRCGVHPGPGTFLFMGWSRFGEARLGCAPR
      220      230      240      *      250      260      *
      290      300      * 310
Innog. FKDFQRMRYRDAQERGLNPCEVGTD (SEQ ID NO:40)
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NsG33  FQEFRRAYEAARAHLHPCEVALH (SEQ ID NO:3)
      270      280      290
```

Fig 5

6/13

```
1  gcttcgccgg ggcggggcgg ccggcgcccc cggctgtccc cgcgcgccgc cggaccgcgc cccgcgcggg cccgcgcggg gcagcgggtg tgagagcccc gactccccgg
101 acgcgcgccg ccgtgccatg ggggttcccc cgcgcggcgt gctctgcgcg ctgtgtctgg ccctctctgg ccgggctgcc cgcgcgcggct actccgagga
>>.....CDS.....>
      m g f p a a a l l c a l c c g l l a p a a r a g y s e
201 gcgctgcagc tggaggggca ggcgcctcac ccaggagccc ggcagcgtgg ggcagctggc cctggcctgt gcgaggggcg cggttgagtg gctgtaccgc
>>.....CDS.....>
      e r c s w r g s g l t q e p g s v g q l a l a c a e g a v e w l y p
301 getggggcgc tgcgctgac cctggggcgc cccgatccca gagcgcggcc cggcatcgcc tgtctgcggc cggttgcggc cttcgcgggc gcccaggtct
>>.....CDS.....>
      a g a l r l t l g g p d p r a r p g i a c l r p v r p f a g a q v
401 tcgcggagcg cgcagggggc gccctggagc tgctgtggc cgagggcccc ggcgcggcag gggcgcgtg cgtgcgctgg ggtccccgcg agcgccgggc
>>.....CDS.....>
      f a e r a g g a l e l l l a e g p g p a g g r c v r w g p r e r r
501 cctcttctcg caggccacgc cgcaccagga catcagccgc cgcgtggcgc ccttcgctt tgagctggc gaggacgggc gccccgagct gcccccgcag
>>.....CDS.....>
      a l f l q a t p h q d i s r r v a a f r f e l r e d g r p e l p p q
601 gccacggtc tcggcgtaga cgggtgcctgc aggccttgc gcgacgtga gctgtcctg gccgcatgca ccaggactt cgtaatcac gggatcatcc
>>.....CDS.....>
      a h g l g v d g a c r p c s d a e l l l a a c t s d f v i h g i i
701 atggggtcac ccattgacgt gagctgcagg agtctgtcat cactgtggtg gcgcgcctg tctccgca gacaccgcg cgtgtccagg cggggcgatc
>>.....CDS.....>
      h g v t h d v e l q e s v i t v v a a r v l r q t p p l f q a g r
801 cggggaccag gggctgacct ccattcgtag cccactgac tgtggcgtcc acccgggcc aggcacctc cttctcatgg gctggagccg ctttggggag
>>.....CDS.....>
      s g d q g l t s i r t p l r c g v h p g p g t f l f m g w s r f g e
901 gcccggtgg gctgtgcccc acgattccag gagtccgccc gtgcctacga ggctgccgt gctgcccacc tccaccctg cgaggtggcg ctgcactgag
>>.....CDS.....>
      a r l g c a p r f q e f r r a y e a a r a a h l h p c e v a l h
1001 gggctgggtg ctggggaggg gctggtagga gggagggtgg gccactgct ttggaggtga tgggactatc aataagaact ctgttcacgc aaaaaaaaaa
1101 aaaaaaaaaa (SEQ ID NO:2)
```

Fig 6

1001 gggctgggtg ctggggaggg gctggtagga gggagggtgg gccactgct ttggaggtga tgggactatc aataagaact ctgttcacgc aaaaaaaaaa (SEQ ID NO:3)

```

1  ccacgcgtcc gccacacgct ccgcgcgtct ttgcgcgctc ttgtgcggcc tccgtgcgc gtcgcgtcac gctgggtact cggaagacgc ctgcagctgg
>>.....CDS.....>
   h a s a h a s a l l c a l c c g l l a a s a h a g y s e d r c s w
101 aggggcagcg gtttgacca ggagcctggc agctgagcct ggactgtact gagggcgcta tcgagtggct gtaccacgct ggggcgctgc
>>.....CDS.....>
   r g s g l t q e p g s v g q l t l d c t e g a i e w l y p a g a l
201 gcctgacct gggcgcccc gatccggca cagggcccag catcgtctgt ctgcgccag agcgccctt cgtgtgtgcc caggtcttcg ctgaacgtat
>>.....CDS.....>
   r l t l g g p d p g t r p s i v c l r p e r p f a g a q v f a e r
301 gacggcaat ctagagtgc tactggcga gggccggac ctggctggg gccgtgcat gcgtgggggt cccgcgagc gccgagcct ttccctgcag
>>.....CDS.....>
   m t g n l e l l a e g p d l a g g r c m r w g p r e r a l f l q
401 gccacaccac acccgacat cagccgcaga gttgctgcct tccgtttga actgcacgag gaccaacgtg cagaaatgtc tcccaggct caaggtcttg
>>.....CDS.....>
   a t p h r d i s r r v a a f r f e l h e d q r a e m s p q a q g l
501 gtgtggatgg tgctgcagg cctgcagtg atgcgagct cctcctggct gcatgcacca gtgattttgt gatccacggg accatccatg gggctgcacca
>>.....CDS.....>
   g v d g a c r p c s d a e l l l a a c t s d f v l h g t i h g v a
601 tgacacagag ctgcaagaat cagtcacac tgtgtgtggt gctcgtgtca tccgccagac actgcacactg ttcaaggag ggagctcgga gggccaaagg
>>.....CDS.....>
   h d t e l q e s v i t v v a r v i r q t l p l f k e g s s e g q g
701 cgggcctcca ttctgacctt gctgcgctgt ggtgtcgtc ctggcccagg ctccttcctc ttcatgggct ggagccgatt tggcgaagct tggctgggct
>>.....CDS.....>
   r a s i r t l l r c g v r p g p g s f l f m g w s r f g e a w l g
801 gtgtccccc ctccaagag ttacgcgtg tctattcagc tgctctcag accatctca accatgtga gatggcactg gactgagaga cctggggagca
>>.....CDS.....>
   c a p r f q e f s r v y s a a l t t h l n p c e m a l d - (SEQ ID NO:8)
901 agccctggat ggaccttctt ctggagatgg ggtgttgggg aggtgtgatgg gaggttgggt gagaagggtg tggctcggat ggcacacctg taccacagct
>>.....CDS.....>
1001 gagctggtag aatactaagt aatctggacc ataaaaaaaa aaaaaaaa (SEQ ID NO:7)

```

Fig 7a

```

1  gggcagccgc gccgcgggct gctcgcgctg cggccccgac cctccccggg cagcagtcgc aggcccccgc ggcgtcccta accatgctgg
   >>CDS.>
   m 1
91  tagccacgct tctttgcgc cttctgttgc gctctctggc cgcgtccgct cagctgggt actcggaaga cgcctgcgc tggaggggca
   >.....CDS.....>
   v a t l l c a l c c g l l a a s a h a g y s e d r c s w r g
181  gcggtttgac ccaggagcct ggcagcgtgg ggcagctgac cctggactgt actgaggcgc ctatcgagt gctgtacca gctggggcgc
   >.....CDS.....>
   s g l t q e p g s v g q l t l d c t e g a i e w l y p a g a
271  tgcgcctgac cctggggcgc ccgcatcgc gcacacggcc cagcatcgtc tgtctgcgc cagaggggcc cttcgtggt gcccaggtct
   >.....CDS.....>
   l r l t l g g p d p g t r p s i v c l r p e r p f a g a q v
361  tcgctgaacg tatgaccgc aatctagagt tgctactggc cagggggccg gacctggctg ggggcgcgtg catgcgctg ggtccccgcg
   >.....CDS.....>
   f a e r m t g n l e l l l a e g p d l a g g r c m r w g p r
451  agcgcgagc ccttttcctg caggccacac cacacgcga catcagcgc agagtgtctg ccttcggtt tgaactgcac gaggaccaac
   >.....CDS.....>
   e r a l f l q a t p h r d l s r r v a a f r f e l h e d q
541  gtgcagaaat gtctccccag gctcaaagtc ttggtgtgga ttgtgcctgc aggccctgca gtgatgcga gctcctcctg gctgcattgca
   >.....CDS.....>
   r a e m s p q a q g l g v d g a c r p c s d a e l l l a a c
631  ccagtgattt tgtgatccac gggaccatcc atggggtcgc ccattgacaca gagctgcaag aatcagtcac cactgtggtg gttgctcgtg
   >.....CDS.....>
   t s d f v i h g t i h g v a h d t e l q e s v i t v v a r
721  tcacccgcca gacctgcca ctgttcaagg aaggagctc ggaggggcca ggccgggccc ccattcgtac cttgctgcgc tgtggtgtgc
   >.....CDS.....>
   v i r q t l p l f k e g s s e g q g r a s i r t l l r c g v
811  gtcctggccc aggtccttc ctcttcattg gctggagccg atttgcgaa gcttggtgg gctgtgctcc ccgttccaa gattcagcc
   >.....CDS.....>
   r p g p g s f l f m g w s r f g e a w l g c a p r f q e f s
901  gtgtctattc agctgtctc acgaccatc tcaaccatg tgagatgga ctggactgag agacctggga gcaagccctg gatggacctt
   >.....CDS.....>
   r v y s a a l t t h l n p c e m a l d - (SEQ ID NO:26)
991  cttctggaga tggggtgtg gggagggtga tgggaggtg ggtgagaagg gttggctcg gatggcatcc tggtaaccac agtgagctgg
1081  tagaatacta agtaactctg accataccag ccactagagt catggcttc tbtggcagc agcataccca gctctgtgc tgcctcactt
1171  tgtctactct ccagtctgct gcccttctaa cccttcttag cctgtgacc agtgagctca tgtttcctc gaattccagg gtgctgctgg
1261  ggttcagagc aacctgccc tagtttggaa gacttgagct aattgtttt tttttgtttg tttttaaagg tggcctgggg
1351  gggggggcaa aca (SEQ ID NO:25)

```

Fig 7b

9/13

```

1  atgctggttag cggcgcttct ctgcgcgctg tgctgcggcc tcttggtgc gtccgtctga gctggctact ccgaggaccg ctgcagctgg aggggcagcg
>>.....CDS>
    m l v a a l l c a l c c g l l a a s a r a g y s e d r c s w r g s
101 gttgacca ggaacctggc agcgtgggc agctgacct ggattgtact gaggtgtcta tcgagtggct gatatcagct ggggcgtgc gcctgactct
>.....CDS>
    g l t q e p g s v g q l t l d c t e g a i e w l y p a g a l r l t
201 agcggtctct gatccgggca cgcggccag catgctctgt ctgcgccaa cacggccctt cgctggtgcc caggtcttcg ctgaacggat ggccggcaac
>.....CDS>
    l g g s d p g t r p s i v c l r p t r p f a g a q v f a e r m a g n
301 ctgagattgc tactggcca gggccaaggc ctggtgggc gccgtgcat gcgtgggt cctgcgagc gccgagcct ttctctgcag gccacgccac
>.....CDS>
    l e l l l a e g q g l a g g r c m r w g p r e r a l f l q a t p
401 accgggacat cagccgcaga gttgctgcct tccaattga actgcacgag gaccaacgtg cagaaatgc tccccaggcc caagggtttg gtgtggatgg
>.....CDS>
    h r d i s r r v a a f q f e l h e d q r a e m s p q a q g f g v d
501 tgcctgcagg ccctgcagtg atgccgagct cctctgact gcattgcac gtgactttgt gatccatggg accatccatg gggctgtcca tgacatggag
>.....CDS>
    g a c r p c s d a e l l l t a c t s d f v i h g t i h g v v h d m e
601 ctgcaagaat cagtcacac tgtgtggccc actcgtgtca tccgccagac actgccactg ttccaggaag ggagctcgga gggccggggc caggcctccg
>.....CDS>
    l q e s v i t v v a t r v i r q t l p l f q e g s s e g r g q a s
701 ttcgtacctt gttgcgtgt ggtgtgcgtc ctggcccagg ctcttctc ttcatgggt ggagccgatt tggcgaagct tggctgggt gcgtccccc
>.....CDS>
    v r t l l r c g v r p g p g s f l f m g w s r f g e a w l g c a p
801 cttccaagag ttcagccgtg tctattcagc tgctctcgc gccaccta acccatgta ggtggcactg gactgagaga cctggggagca agccctggat
>.....CDS>
    r f q e f s r v y s a a l a a h l n p c e v a l d - (SEQ ID NO:13)
901 ggatcttct ctgggggatgg ggtgttggg aggggtgata ggggggtggg tgggaaggggt gtgggtcaga tggcatcctg gtaccacag tgaggttgga
1001 gaatactaaa taacctggat cacacc (SEQ ID NO:12)

```

Fig 8